

STN/EAR scan strategy

(FILE 'HOME' ENTERED AT 16:48:10 ON 10 FEB 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 16:48:19 ON 10 FEB
2005

L1 15 S PICHIA (2N) FINLANDICA
L2 1 S L1 AND DEHYDROGENASE
L3 76 S PICHIA (2N) JADINII
L4 11 S L3 AND DEHYDROGENASE
L5 5 DUP REM L4 (6 DUPLICATES REMOVED)
L6 1 S L5 AND OCTANOL
L7 703 S CANDIDA AND DEHYDROGENASE AND (ALCOHOL OR OCTANOL)
L8 86 S L7 AND UTILIS
L9 62 DUP REM L8 (24 DUPLICATES REMOVED)
L10 6 S L9 AND KETONE
L11 6 DUP REM L10 (0 DUPLICATES REMOVED)
L12 3 S L9 AND OCTANOL
L13 24 S (PICHIA OR CANDIDA OR OGATAEA) AND DEHYDROGENASE AND OCTANOL
L14 14 DUP REM L13 (10 DUPLICATES REMOVED)
L15 1 S (PICHIA OR CANDIDA OR OGATAEA) AND DEHYDROGENASE AND (HALOACE

=> s (pichia or candida or ogataea) and dehydrogenase and (haloacetoacetic or chloroacetoacetic or octanol or hydroxybutyric)

L16 27 (PICHIA OR CANDIDA OR OGATAEA) AND DEHYDROGENASE AND (HALOACETOACETIC OR CHLOROACETOACETIC OR OCTANOL OR HYDROXYBUTYRIC

	Type	Hits	Search Text
1	BRS	3	"6706507"
2	BRS	13	octanol near2 dehydrogenase
3	BRS	17	octanol near10 dehydrogenase
4	BRS	48	2-octanol and dehydrogenase
5	BRS	3	S84 and haloacetoacetic
6	BRS	23	S84 and (optically)
7	BRS	541	(R) near10 dehydrogenase
8	BRS	298	S87 and secondary
9	BRS	14	S88 and octanol
10	BRS	0	pichia near5 "11328"
11	BRS	5	pichia near10 "11328"
12	BRS	29	S92 and alcohol
13	BRS	36	pichia near2 dehydrogenase
14	BRS	405	(candida or pichia or ogataea) and octanol
15	BRS	98	S94 and dehydrogenase
16	BRS	79	S95 and (dna or polynucleotide or gene or cdna or cloning)
17	BRS	78	S96 and (ketone or alcohol)
18	BRS	12	S96 and (finlandica or jadinii or utilis or wicerhamii)
19	BRS	7	S96 and (chloroacetoacetic or haloacetoacetic or hydroxybutyric)
20	BRS	3160	dehydrogenase and (chloroacetoacetic or haloacetoacetic or hydroxybutyric)
21	BRS	9285	(chloroacetoacetic or haloacetoacetic or hydroxybutyric)
22	BRS	1666	(finlandica or jadinii or utilis or wicerhamii)
23	BRS	3	S101 and S102 and octanol
24	BRS	30939	(candida or pichia or ogataea)
25	BRS	2856	S101 and S104
26	BRS	14	S105 and octanol
27	BRS	49	S102 and (S101 or octanol)
28	BRS	20	S107 and (polynucleotide or dna)
29	BRS	11257	(secondary or alcohol or octanol) near5 dehydrogenase
30	BRS	11172	(secondary or alcohol or octanol) near3 dehydrogenase
31	BRS	2641	S110 and (S101 or octanol)

32	BRS	2558	S111 and (DNA or polynucleotide)
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	Type	Hits	Search Text
33	BRS	11056	(secondary or alcohol or octanol) near2 dehydrogenase
34	BRS	2641	S113 and (S101 or octanol)
35	BRS	2558	S114 and (dna or polynucleotide)
36	BRS	35	S115 and (method near10 alcohol)
37	BRS	213111	yamamoto
38	BRS	0	S117 and dehycrogénase
39	BRS	2769	S117 and dehydrogenase
40	BRS	420	yamamoto and kawada
41	BRS	35	yamamoto and kawada and matsuyama
42	BRS	11053	(secondary or alcohol) near2 dehydrogenase
43	BRS	86	S122 near6 (r)
44	BRS	43	S123 and (nadh or nad)
45	BRS	32	S124 and ketone
46	BRS	1267	R-configuration
47	BRS	34	S126 near10 (alcohol or octanol)
48	BRS	3	S127 and dehydrogenase

	Type	Hits	Search Text
1	BRS	3	"6706507"
2	BRS	13	octanol near2 dehydrogenase
3	BRS	17	octanol near10 dehydrogenase
4	BRS	48	2-octanol and dehydrogenase
5	BRS	3	S84 and haloacetoacetic
6	BRS	23	S84 and (optically)
7	BRS	541	(R)near10 dehydrogenase
8	BRS	298	S87 and secondary
9	BRS	14	S88 and octanol
10	BRS	0	pichia near5 "11328"
11	BRS	5	pichia near10 "11328"
12	BRS	29	l1 and alcohol
13	BRS	36	pichia near2 dehydrogenase

L14 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 1
AN 1997:759214 CAPLUS
DN 128:127143
TI A novel reactor concept for the enzymic reduction of poorly soluble ketones
AU Liese, A.; Zelinski, T.; Kula, M.-R.; Kierkels, H.; Karutz, M.; Kragl, U.; Wandrey, C.
CS Forschungszentrum Julich GmbH, Institute of Biotechnology, D-52425 Julich, Germany
SO Journal of Molecular Catalysis B: Enzymatic (1998), 4(1-2), 91-99
CODEN: JMCEF8; ISSN: 1381-1177
PB Elsevier Science B.V.
DT Journal
LA English
AB Redns. of poorly soluble ketones often suffer from low total turnover nos. conferring to the coenzyme and large vols. which are needed for the conversion. The novel emulsion membrane reactor overcomes these limitations. From an emulsion consisting of an organic substrate and an aqueous buffer phase, the aqueous phase is separated selectively by using a hydrophilic ultrafiltration membrane and fed to a subsequent enzyme membrane reactor. The product outflow is recirculated to the emulsion stirred vessel and, due to the partition coeffs., the aqueous phase is recharged with substrate while the product is extracted. This new reactor concept will be compared to the classical enzyme membrane reactor. The latter was operated under the same conditions over a period of 4 mo at a space-time yield of 21.2 g l⁻¹ day⁻¹. As a model system, the enantioselective reduction of 2-octanone to (S)-2-octanol (ee > 99.5) is used, carried out by a carbonyl reductase from *Candida parapsilosis*. NADH is regenerated by formate dehydrogenase from *Candida boidinii*. In comparison to the classical enzyme membrane reactor, the total turnover number could be increased by a factor 9 using the novel emulsion membrane reactor.

L17 ANSWER 12 OF 17 MEDLINE on STN DUPLICATE 3
AN 95045575 MEDLINE
DN PubMed ID: 7957234
TI Structure of the *Drosophila melanogaster* glutathione-dependent formaldehyde **dehydrogenase/octanol dehydrogenase** gene (class III alcohol **dehydrogenase**).
Evolutionary pathway of the alcohol **dehydrogenase** genes.
AU Luque T; Atrian S; Danielsson O; Jornvall H; Gonzalez-Duarte R
CS Department of Genetics, Faculty of Biology, University of Barcelona,
Spain.
SO European journal of biochemistry / FEBS, (1994 Nov 1) 225 (3) 985-93.
Journal code: 0107600. ISSN: 0014-2956.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U07799
EM 199412
ED Entered STN: 19950110
Last Updated on STN: 19960129
Entered Medline: 19941221
AB The glutathione-dependent formaldehyde **dehydrogenase** gene (*gfd*) of *Drosophila melanogaster* encodes an enzyme that is active toward S-hydroxymethylglutathione, an adduct of formaldehyde with glutathione, and also with long-chain primary alcohols, both properties typical of class III alcohol **dehydrogenases**. *gfd* hybridizes at the 86D division of the third chromosome, in agreement with the known location of the *Drosophila octanol dehydrogenase* gene (*odh*). *gfd/odh* was isolated from a lambda EMBL-4 genomic library and consists of three exons (with coding segments of 21, 90 and 1029 bp) and two introns (69 bp and 70 bp, respectively). The introns are small in size like the *Drosophila* interrupting sequences and are located at the 5' end of the coding region. Comparisons with the homologous genes of *Saccharomyces*, *Candida* and humans provide information on the evolution of the class III alcohol **dehydrogenases**. Moreover, results from analysis of exon/intron distributions in eleven **dehydrogenases** are compatible with the hypothesis of intron loss accounting for aspects of the present structure of these genes.



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#9	Search Field: Title/Abstract, Limits: Publication Date to 2000	09:59:50	13077763
#7	Search alcohol dehydrogenase pichia octanol Field: Title/Abstract, Limits: Publication Date to 2000	09:59:29	1
#6	Search alcohol dehydrogenase pichia Field: Title/Abstract, Limits: Publication Date to 2000	09:59:13	22
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Feb 8 2005 07:27:47